SEQUENCE LISTING

<110> CANFIELD, William
KORNFELD, Stuart

<120> EXPRESSION OF LYSOSOMAL HYDROLASE IN CELLS EXPRESSING PRO-N-ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANIDASE

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195 200 205

Arg Gly Tyr Leu Thr Thr Asp Lys Glu Val Pro Gly Leu Val Leu Met
210 215 220

Gln Asp Leu Ala Phe Leu Ser Gly Phe Pro Pro Thr Phe Lys Glu Thr
225 230 235 240

Asn Gln Leu Lys Thr Lys Leu Pro Glu Asn Leu Ser Ser Lys Val Lys
245 250 255

Leu Leu Gln Leu Tyr Ser Glu Ala Ser Val Ala Leu Leu Lys Leu Asn
260 265 270

Asn Pro Lys Asp Phe Gln Glu Leu Asn Lys Gln Thr Lys Lys Asn Met
275 280 285

Thr Ile Asp Gly Lys Glu Leu Thr Ile Ser Pro Ala Tyr Leu Leu Trp
290 295 300

Asp Leu Ser Ala Ile Ser Gln Ser Lys Gln Asp Glu Asp Ile Ser Ala
305 310 315 320

Ser Arg Phe Glu Asp Asn Glu Glu Leu Arg Tyr Ser Leu Arg Ser Ile
325 330 335

Glu Arg His Ala Pro Trp Val Arg Asn Ile Phe Ile Val Thr Asn Gly
340 345 350

Gln Ile Pro Ser Trp Leu Asn Leu Asp Asn Pro Arg Val Thr Ile Val
355 360 365

Thr His Gln Asp Val Phe Arg Asn Leu Ser His Leu Pro Thr Phe Ser
370 375 380

Ser Pro Ala Ile Glu Ser His Ile His Arg Ile Glu Gly Leu Ser Gln
385 390 395 400

Lys Phe Ile Tyr Leu Asn Asp Asp Val Met Phe Gly Lys Asp Val Trp
405 410 415

Pro Asp Asp Phe Tyr Ser His Ser Lys Gly Gln Lys Val Tyr Leu Thr
420 425 430

Trp Pro Val Pro Asn Cys Ala Glu Gly Cys Pro Gly Ser Trp Ile Lys
435 440 445

Asp Gly Tyr Cys Asp Lys Ala Cys Asn Asn Ser Ala Cys Asp Trp Asp
450 455 460

Gly Gly Asp Cys Ser Gly Asn Ser Gly Gly Ser Arg Tyr Ile Ala Gly
465 470 475 480

Gly Gly Gly Thr Gly Ser Ile Gly Val Gly His Pro Trp Gln Phe Gly
485 490 495

Gly Gly Ile Asn Ser Val Ser Tyr Cys Asn Gln Gly Cys Ala Asn Ser
500 505 510

Trp Leu Ala Asp Lys Phe Cys Asp Gln Ala Cys Asn Val Leu Ser Cys
515 520 525

Gly Phe Asp Ala Gly Asp Cys Gly Gln Asp His Phe His Glu Leu Tyr
530 535 540

Lys Val Ile Leu Leu Pro Asn Gln Thr His Tyr Ile Ile Pro Lys Gly
545 550 555 560

Glu Cys Leu Pro Tyr Phe Ser Phe Ala Glu Val Ala Lys Arg Gly Val
565 570 575

Glu Gly Ala Tyr Ser Asp Asn Pro Ile Ile Arg His Ala Ser Ile Ala
580 585 590

Asn Lys Trp Lys Thr Ile His Leu Ile Met His Ser Gly Met Asn Ala
595 600 605

Thr Thr Ile His Phe Asn Leu Thr Phe Gln Asn Thr Asn Asp Glu Glu
610 615 620

Phe Lys Met Gln Ile Thr Val Glu Val Asp Thr Arg Glu Gly Pro Lys
625 630 635 640

Leu Asn Ser Thr Ala Gln Lys Gly Tyr Glu Asn Leu Val Ser Pro Ile
645 650 655

Thr Leu Leu Pro Glu Ala Glu Ile Leu Phe Glu Asp Ile Pro Lys Glu
660 665 670

Lys Arg Phe Pro Lys Phe Lys Arg His Asp Val Asn Ser Thr Arg Arg
675 680 685

Ala Gln Glu Glu Val Lys Ile Pro Leu Val Asn Ile Ser Leu Leu Pro
690 695 700

Lys Asp Ala Gln Leu Ser Leu Asn Thr Leu Asp Leu Gln Leu Glu His
705 710 715 720

Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu Ser Lys Ser Ala Leu Leu
725 730 735

Arg Ser Phe Leu Met Asn Ser Gln His Ala Lys Ile Lys Asn Gln Ala
740 745 750

Ile Ile Thr Asp Glu Thr Asn Asp Ser Leu Val Ala Pro Gln Glu Lys
755 760 765

Gln Val His Lys Ser Ile Leu Pro Asn Ser Leu Gly Val Ser Glu Arg
770 775 780

Leu Gln Arg Leu Thr Phe Pro Ala Val Ser Val Lys Val Asn Gly His
785 790 795 800

Asp Gln Gly Gln Asn Pro Pro Leu Asp Leu Glu Thr Thr Ala Arg Phe

805 810 815

Arg Val Glu Thr His Thr Gln Lys Thr Ile Gly Gly Asn Val Thr Lys
820 825 830

Glu Lys Pro Pro Ser Leu Ile Val Pro Leu Glu Ser Gln Met Thr Lys
835 840 845

Glu Lys Lys Ile Thr Gly Lys Glu Lys Glu Asn Ser Arg Met Glu Glu
850 855 860

Asn Ala Glu Asn His Ile Gly Val Thr Glu Val Leu Leu Gly Arg Lys
865 870 875 880

Leu Gln His Tyr Thr Asp Ser Tyr Leu Gly Phe Leu Pro Trp Glu Lys
885 890 895

Lys Lys Tyr Phe Gln Asp Leu Leu Asp Glu Glu Glu Ser Leu Lys Thr
900 905 910

Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn Thr Gly Arg Gln Leu Lys
915 920 925

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<212> PRT
<213> Homo sapiens

<400> 5

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Lys Phe Gly Phe Thr Ser Arg Lys Val Pro Ala His Met Pro His Met
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Ile Asp Arg Ile Val Met Gln Glu Leu Gln Asp Met Phe Pro Glu Glu
35 40 45

Phe Asp Lys Thr Ser Phe His Lys Val Arg His Ser Glu Asp Met Gln
50 55 60

Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met Ser Ala Val Gln Pro Leu
65 70 75 80

Asn Ile Ser Gln Val Phe Asp Glu Val Asp Thr Asp Gln Ser Gly Val
85 90 95

Leu Ser Asp Arg Glu Ile Arg Thr Leu Ala Thr Arg Ile His Glu Leu
100 105 110

Pro Leu Ser Leu Gln Asp Leu Thr Gly Leu Glu His Met Leu Ile Asn
115 120 125

Cys Ser Lys Met Leu Pro Ala Asp Ile Thr Gln Leu Asn Asn Ile Pro
130 135 140

Pro Thr Gln Glu Ser Tyr Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys
145 150 155 160

Ser Leu Val Thr Asn Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala
165 170 175

Tyr Lys Asp Lys Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu Glu
180 185 190

Ile Ala Phe Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln
195 200 205

Leu Asp Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp
210 215 220

Asn Ile Asp His Asn His Lys Asp Ala Gln Thr Val Lys Ala Val Leu
225 230 235 240

Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu Leu
245 250 255

Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu Gln Glu
260 265 270

Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe Trp Thr His Cys Val Leu
275 280 285

Ala Thr Leu Ile Met Phe Thr Ile Phe Ser Phe Phe Ala Glu Gln Leu
290 295 300

Ile Ala Leu Lys Arg Lys Ile Phe Pro Arg Arg Arg Ile His Lys Glu
305 310 315 320

Ala Ser Pro Asn Arg Ile Arg Val
325

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<211> 1219
<212> DNA
<213> Homo sapiens

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ccaacgcgtt tggggtgaac aacccgttct tgcctcaggc cagtcgcctc caggccaaga 180

gggatccttc acccgtgtct ggacccgtgc atctcttccg actctcgggc aagtgcttca 240

gcctggtgga gtccacgtac aagtatgagt tctgcccgtt ccacaacgtg acccagcacg 300

agcagacctt ccgctggaac gcctacagtg ggatcctcgg catctggcac gagtgggaga 360

tcgccaacaa caccttcacg ggcatgtgga tgagggacgg tgacgcctgc cgttcccgga 420

gccggcagag caaggtggag ctggcgtgtg gaaaaagcaa ccggctggcc catgtgtccg 480

agccgagcac ctgcgtctat gcgctgacgt tcgagacccc cctcgtctgc cacccccacg 540

ccttgctagt gtacccaacc ctgccagagg ccctgcagcg gcagtgggac caggtagagc 600

aggacctggc cgatgagctg atcacccccc agggccatga gaagttgctg aggacacttt 660

ttgaggatgc tggctactta aagaccccag aagaaaatga acccacccag ctggagggag 720

gtcctgacag cttggggttt gagaccctgg aaaactgcag gaaggctcat aaagaactct 780

caaaggagat caaaaggctg aaaggtttgc tcacccagca cggcatcccc tacacgaggc 840

ccacagaaac ttccaacttg gagcacttgg gccacgagac gcccagagcc aagtctccag 900

agcagctgcg gggtgaccca ggactgcgtg ggagtttgtg accttgtggt gggagagcag 960

aggtggacgc ggccgagagc cctacagaga agctggctgg taggacccgc aggaccagct 1020

gaccaggctt gtgctcagag aagcagacaa aacaaagatt caaggtttta attaattccc 1080

atactgataa aaataactcc atgaattctg taaaccattg cataaatgct atagtgtaaa 1140

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<210> 7
<211> 305
<212> PRT
<213> Homo sapiens

<400> 7

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Met Ala Ala Gly Leu Ala Arg Leu Leu Leu Leu Leu Gly Leu Ser Ala
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Gly Gly Pro Ala Pro Ala Gly Ala Ala Lys Met Lys Val Val Glu Glu
            20                  25                  30

Pro Asn Ala Phe Gly Val Asn Asn Pro Phe Leu Pro Gln Ala Ser Arg
        35                  40                  45

Leu Gln Ala Lys Arg Asp Pro Ser Pro Val Ser Gly Pro Val His Leu
    50                  55                  60

Phe Arg Leu Ser Gly Lys Cys Phe Ser Leu Val Glu Ser Thr Tyr Lys
65                  70                  75                  80

Tyr Glu Phe Cys Pro Phe His Asn Val Thr Gln His Glu Gln Thr Phe
                85                  90                  95

Arg Trp Asn Ala Tyr Ser Gly Ile Leu Gly Ile Trp His Glu Trp Glu
            100                 105                 110

Ile Ala Asn Asn Thr Phe Thr Gly Met Trp Met Arg Asp Gly Asp Ala
        115                 120                 125

Cys Arg Ser Arg Ser Arg Gln Ser Lys Val Glu Leu Ala Cys Gly Lys
    130                 135                 140

Ser Asn Arg Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr Ala
145                 150                 155                 160

Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ala Leu Leu Val
                165                 170                 175

Tyr Pro Thr Leu Pro Glu Ala Leu Gln Arg Gln Trp Asp Gln Val Glu
            180                 185                 190

Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln Gly His Glu Lys Leu
        195                 200                 205
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Leu Arg Thr Leu Phe Glu Asp Ala Gly Tyr Leu Lys Thr Pro Glu Glu
210 215 220

Asn Glu Pro Thr Gln Leu Glu Gly Gly Pro Asp Ser Leu Gly Phe Glu
225 230 235 240

Thr Leu Glu Asn Cys Arg Lys Ala His Lys Glu Leu Ser Lys Glu Ile
245 250 255

Lys Arg Leu Lys Gly Leu Leu Thr Gln His Gly Ile Pro Tyr Thr Arg
260 265 270

Pro Thr Glu Thr Ser Asn Leu Glu His Leu Gly His Glu Thr Pro Arg
275 280 285

Ala Lys Ser Pro Glu Gln Leu Arg Gly Asp Pro Gly Leu Arg Gly Ser
290 295 300

Leu
305

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<212> DNA
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gacgtggttt acacctgggt gaatggcact gaccttgaac tgctaaagga gctacagcag 300

gtccgagagc acatggagga agagcagaga gccatgcggg aaaccctcgg gaagaacaca 360

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gctggaccgt ttaagggagg ccagcaaaca gatgtttgga gagcctactt gacaacagac 660

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accttcaagg agacgagtca actgaagaca aagctgccaa gaaaagcttt ccctctaaaa 780

ataaagctgt tgcggctgta ctcggaggcc agtgtcgctc ttctgaaatt gaataatccc 840

aagggtttcc aagagctgaa caagcagacc aagaagaaca tgaccatcga tgggaaggaa 900

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gaagcatact acgaccccaa cctgcctccg gtcactaaga gtcttgtcac caactgtaag 3240

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aaaaaaaaa 5229

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<212> PRT
<213> Mus musculus

<400> 9

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Ser Ala Phe Gln Phe Gly Glu Val Val Leu Glu Trp Ser Arg Asp Gln
35 40 45

Tyr His Val Leu Phe Asp Ser Tyr Arg Asp Asn Ile Ala Gly Lys Ser
50 55 60

Phe Gln Asn Arg Leu Cys Leu Pro Met Pro Ile Asp Val Val Tyr Thr
65 70 75 80

Trp Val Asn Gly Thr Asp Leu Glu Leu Leu Lys Glu Leu Gln Gln Val
85 90 95

Arg Glu His Met Glu Glu Glu Gln Arg Ala Met Arg Glu Thr Leu Gly
100 105 110

Lys Asn Thr Thr Glu Pro Thr Lys Lys Ser Glu Lys Gln Leu Glu Cys
115 120 125

Leu Leu Thr His Cys Ile Lys Val Pro Met Leu Val Leu Asp Pro Ala
130 135 140

Leu Pro Ala Thr Ile Thr Leu Lys Asp Leu Pro Thr Leu Tyr Pro Ser
145 150 155 160

Phe His Ala Ser Ser Asp Met Phe Asn Val Ala Lys Pro Lys Asn Pro
165 170 175

Ser Thr Asn Val Pro Val Val Val Phe Asp Thr Thr Lys Asp Val Glu
180 185 190

Asp Ala His Ala Gly Pro Phe Lys Gly Gly Gln Gln Thr Asp Val Trp
195 200 205

Arg Ala Tyr Leu Thr Thr Asp Lys Asp Ala Pro Gly Leu Val Leu Ile
210 215 220

Gln Gly Leu Ala Phe Leu Ser Gly Phe Pro Pro Thr Phe Lys Glu Thr
225 230 235 240

Ser Gln Leu Lys Thr Lys Leu Pro Arg Lys Ala Phe Pro Leu Lys Ile
245 250 255

Lys Leu Leu Arg Leu Tyr Ser Glu Ala Ser Val Ala Leu Leu Lys Leu

260 265 270

Asn Asn Pro Lys Gly Phe Gln Glu Leu Asn Lys Gln Thr Lys Lys Asn
275 280 285

Met Thr Ile Asp Gly Lys Glu Leu Thr Ile Ser Pro Ala Tyr Leu Leu
290 295 300

Trp Asp Leu Ser Ala Ile Ser Gln Ser Lys Gln Asp Glu Asp Ala Ser
305 310 315 320

Ala Ser Arg Phe Glu Asp Asn Glu Glu Leu Arg Tyr Ser Leu Arg Ser
325 330 335

Ile Glu Arg His Ala Pro Trp Val Arg Asn Ile Phe Ile Val Thr Asn
340 345 350

Gly Gln Ile Pro Ser Trp Leu Asn Leu Asp Asn Pro Arg Val Thr Ile
355 360 365

Val Thr His Gln Asp Ile Phe Gln Asn Leu Ser His Leu Pro Thr Phe
370 375 380

Ser Ser Pro Ala Ile Glu Ser His Ile His Arg Ile Glu Gly Leu Ser
385 390 395 400

Gln Lys Phe Ile Tyr Leu Asn Asp Asp Val Met Phe Gly Lys Asp Val
405 410 415

Trp Pro Asp Asp Phe Tyr Ser His Ser Lys Gly Gln Lys Val Tyr Leu
420 425 430

Thr Trp Pro Val Pro Asn Cys Ala Glu Gly Cys Pro Gly Ser Trp Ile
435 440 445

Lys Asp Gly Tyr Cys Asp Lys Ala Cys Asn Thr Ser Pro Cys Asp Trp
450 455 460

Asp Gly Gly Asn Cys Ser Gly Asn Thr Ala Gly Asn Arg Phe Val Ala
465 470 475 480

Arg Gly Gly Gly Thr Gly Asn Ile Gly Ala Gly Gln His Trp Gln Phe
485 490 495

Gly Gly Gly Ile Asn Thr Ile Ser Tyr Cys Asn Gln Gly Cys Ala Asn
500 505 510

Ser Trp Leu Ala Asp Lys Phe Cys Asp Gln Ala Cys Asn Val Leu Ser
515 520 525

Cys Gly Phe Asp Ala Gly Asp Cys Gly Gln Asp His Phe His Glu Leu
530 535 540

Tyr Lys Val Thr Leu Leu Pro Asn Gln Thr His Tyr Val Val Pro Lys
545 550 555 560

Gly Glu Tyr Leu Ser Tyr Phe Ser Phe Ala Asn Ile Ala Arg Lys Arg
565 570 575

Ile Glu Gly Thr Tyr Ser Asp Asn Pro Ile Ile Arg His Ala Ser Ile
580 585 590

Ala Asn Lys Trp Lys Thr Leu His Leu Ile Met Pro Gly Gly Met Asn
595 600 605

Ala Thr Thr Ile Tyr Phe Asn Leu Thr Leu Gln Asn Ala Asn Asp Glu
610 615 620

Glu Phe Lys Ile Gln Ile Ala Val Glu Val Asp Thr Arg Glu Ala Pro
625 630 635 640

Lys Leu Asn Ser Thr Thr Gln Lys Ala Tyr Glu Ser Leu Val Ser Pro
645 650 655

Val Thr Pro Leu Pro Gln Ala Asp Val Pro Phe Glu Asp Val Pro Lys
660 665 670

Glu Lys Arg Phe Pro Lys Ile Arg Arg His Asp Val Asn Ala Thr Gly
675 680 685

Arg Phe Gln Glu Glu Val Lys Ile Pro Arg Val Asn Ile Ser Leu Leu
690 695 700

Pro Lys Glu Ala Gln Val Arg Leu Ser Asn Leu Asp Leu Gln Leu Glu
705 710 715 720

Arg Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu Ser Lys Ser Ala Leu
725 730 735

Leu Arg Ser Phe Leu Gly Asn Ser Leu Asp Thr Lys Ile Lys Pro Gln
740 745 750

Ala Arg Thr Asp Glu Thr Lys Gly Asn Leu Glu Val Pro Gln Glu Asn
755 760 765

Pro Ser His Arg Arg Pro His Gly Phe Ala Gly Glu His Arg Ser Glu
770 775 780

Arg Trp Thr Ala Pro Ala Glu Thr Val Thr Val Lys Gly Arg Asp His
785 790 795 800

Ala Leu Asn Pro Pro Pro Val Leu Glu Thr Asn Ala Arg Leu Ala Gln
805 810 815

Pro Thr Leu Gly Val Thr Val Ser Lys Glu Asn Leu Ser Pro Leu Ile
820 825 830

Val Pro Pro Glu Ser His Leu Pro Lys Glu Glu Glu Ser Asp Arg Ala
835 840 845

Glu Gly Asn Ala Val Pro Val Lys Glu Leu Val Pro Gly Arg Arg Leu
850 855 860

Gln Gln Asn Tyr Pro Gly Phe Leu Pro Trp Glu Lys Lys Lys Tyr Phe
865 870 875 880

Gln Asp Leu Leu Asp Glu Glu Glu Ser Leu Lys Thr Gln Leu Ala Tyr
885 890 895

Phe Thr Asp Arg Lys His Thr Gly Arg Gln Leu Lys
900 905

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<400> 10

Asp Thr Phe Ala Asp Ser Leu Arg Tyr Val Asn Lys Ile Leu Asn Ser

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1               5                  10                  15

Lys Phe Gly Phe Thr Ser Arg Lys Val Pro Ala His Met Pro His Met
            20                  25                  30

Ile Asp Arg Ile Val Met Gln Glu Leu Gln Asp Met Phe Pro Glu Glu
        35                  40                  45

Phe Asp Lys Thr Ser Phe His Lys Val Arg His Ser Glu Asp Met Gln
    50                  55                  60

Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met Ser Ala Val Gln Pro Leu
65                  70                  75                  80

Asn Ile Ser Gln Val Phe His Glu Val Asp Thr Asp Gln Ser Gly Val
                85                  90                  95

Leu Ser Asp Arg Glu Ile Arg Thr Leu Ala Thr Arg Ile His Asp Leu
            100                 105                 110

Pro Leu Ser Leu Gln Asp Leu Thr Gly Leu Glu His Met Leu Ile Asn
        115                 120                 125

Cys Ser Lys Met Leu Pro Ala Asn Ile Thr Gln Leu Asn Asn Ile Pro
    130                 135                 140

Pro Thr Gln Glu Ala Tyr Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys
145                 150                 155                 160

Ser Leu Val Thr Asn Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala
                165                 170                 175

Tyr Lys Asp Lys Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu Glu
            180                 185                 190

Ile Ala Phe Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln
        195                 200                 205

Leu Asp Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp
    210                 215                 220

Asn Ile Asp His Asn His Lys Asp Ala Arg Thr Val Lys Ala Val Leu
225                 230                 235                 240
```

Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu Leu
245 250 255

Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu Gln Glu
260 265 270

Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe Trp Thr His Cys Val Leu
275 280 285

Ala Thr Leu Ile Ile Phe Thr Ile Phe Ser Phe Phe Ala Glu Gln Ile
290 295 300

Ile Ala Leu Lys Arg Lys Ile Phe Pro Arg Arg Arg Ile His Lys Glu
305 310 315 320

Ala Ser Pro Asp Arg Ile Arg Val
325

<210> 11
<211> 2070
<212> DNA
<213> Mus musculus

<220>
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<222> (186)..(186)
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cattcgggtg agcggatcac ggtcctgcgg cttggggacc gagcctggct ggttcttctg 180

accttntcaa ttccataggc tgaataaccc gttcttgccc caggcaagcc gccttcagcc 240

caagagagag ccttcagctg tatcccgcaa attaagagaa attaatttca aacgatttag 300

aaagtattct agccaggcga tgatggcgca cgcctttaat cccagcactt gggaggcaga 360

ggcaggcaga tttccgagtt caaggccatc agaactgact gtacatctta gtacagttta 420

gcatgtgatc agagatctga atcacaaagc tgggcctgcg tggtaaagca ggtcctttct 480

aataaggttg cagtttagat tttctttctt aactctttta ttctttgaga cagggtttct 540

caacagtggg tgtcctggaa ctcacttttg taaaccaggc tgcccttaaa ctcacaaagc 600

tctgtcagcc tctgcctcct gagtgctggg attaaaggtc cacaccctgt tcattcattt 660

ttaattttg agactgggtc tcattatgtg gccctagaca gatactgaga gcctcctcca 720

caggaacaag catgggaatc ctgccacaga caaccagttc tgtggtctgg agatgagttt 780

gtcagtccct aggagttagg tcagcctgcc tctgcattcc caataattta ggaaaggagc 840

ttggggcgtt ctggccttga tggttagtgc cctcctgcca accttagctt ccagctttag 900

gggtagcaga gtttataccg atgctaaact gctgttgtgt tcttccccag ggcccctgca 960

tctcttcaga cttgctggca agtgctttag cctagtggag tccacgtgag tgccaggctg 1020

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tatgaattct gccctttcca caacgtcacc cagcacgagc agaccttccg ctggaatgcc 1140

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atgtggatga ctgatgggga ctcctgccac tcccggagcc ggcagagcaa ggtggagctc 1260

acctgtggaa agatcaaccg actggcccac gtgtctgagc caagcacctg tgtctatgca 1320

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tcagaagccc tgcagcagcc cttggaccag gtggaacagg acctggcaga tgaactgatc 1440

acaccacagg gctatgagaa gttgctaagg gtacttttg aggatgctgg ctacttaaag 1500

gtcccaggag aaacccatcc cacccagctg gcaggaggtt ccaagggcct ggggcttgag 1560

actctggaca actgtagaaa ggcacatgca gagctgtcac aggaggtaca aagactgacg 1620

agtctgctgc aacagcatgg aatcccccac actcagccca caggtcagtc tgcctgccct 1680

ggtcagctgc cagccactcc ggggcctgca gcactggggc agatctttat tgctacccat 1740

tctggcagaa accactcact ctcagcacct gggtcagcag ctccccatag gtgcaatcgc 1800

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tggtgtagac acggcttctt ttggcatatt ctagatcaga cagtgtcact gacaaacaag 1980

agggacctgc tggccagcct ttgttgtgcc caaagatcca gacaaaataa agattcaaag 2040

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<210> 12
<211> 307
<212> PRT
<213> Mus musculus

<400> 12

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Met Ala Gly Arg Leu Ala Gly Phe Leu Met Leu Leu Gly Leu Ala Ser
1               5                  10                  15

Gln Gly Pro Ala Pro Ala Cys Ala Gly Lys Met Lys Val Val Glu Glu
            20                  25                  30

Pro Asn Thr Phe Gly Leu Asn Asn Pro Phe Leu Pro Gln Ala Ser Arg
        35                  40                  45

Leu Gln Pro Lys Arg Glu Pro Ser Ala Val Ser Gly Pro Leu His Leu
    50                  55                  60

Phe Arg Leu Ala Gly Lys Cys Phe Ser Leu Val Glu Ser Thr Tyr Lys
65                  70                  75                  80

Tyr Glu Phe Cys Pro Phe His Asn Val Thr Gln His Glu Gln Thr Phe
                85                  90                  95

Arg Trp Asn Ala Tyr Ser Gly Ile Leu Gly Ile Trp His Glu Trp Glu
            100                 105                 110

Ile Ile Asn Asn Thr Phe Lys Gly Met Trp Met Thr Asp Gly Asp Ser
        115                 120                 125

Cys His Ser Arg Ser Arg Gln Ser Lys Val Glu Leu Thr Cys Gly Lys
    130                 135                 140

Ile Asn Arg Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr Ala
145                 150                 155                 160

Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ser Leu Leu Val
                165                 170                 175

Tyr Pro Thr Leu Ser Glu Ala Leu Gln Gln Arg Leu Asp Gln Val Glu
            180                 185                 190

Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln Gly Tyr Glu Lys Leu
        195                 200                 205

Leu Arg Val Leu Phe Glu Asp Ala Gly Tyr Leu Lys Val Pro Gly Glu
    210                 215                 220
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Thr His Pro Thr Gln Leu Ala Gly Gly Ser Lys Gly Leu Gly Leu Glu
225 230 235 240

Thr Leu Asp Asn Cys Arg Lys Ala His Ala Glu Leu Ser Gln Glu Val
245 250 255

Gln Arg Leu Thr Ser Leu Leu Gln Gln His Gly Ile Pro His Thr Gln
260 265 270

Pro Thr Glu Thr Thr His Ser Gln His Leu Gly Gln Gln Leu Pro Ile
275 280 285

Gly Ala Ile Ala Ala Glu His Leu Arg Ser Asp Pro Gly Leu Arg Gly
290 295 300

Asn Ile Leu
305

<210> 13
<211> 460
<212> DNA
<213> Rattus rattus

<400> 13
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taaccccaaa ggtttccccg agctgaacaa gcagaccaag aagaacatga gcatcagtgg 180

gaaggaactg gccatcagcc ctgcctatct gctgtgggac ctgagcgcca tcagccagtc 240

caagcaggat gaagatgtgt ctgccagccg cttcgaggat aacgaagagc tgaggtactc 300

actgagatct atcgagagac atgattccat gagtccttta tgaattctgg ccatatcttc 360

aatcatgatc tcagtagtat tcctctgaaa tggcacacat ttttctaatg agaacttgaa 420

atgtaaatat tgtgtttgtg ctgtaaattt tgtgtatttc 460

<210> 14
<211> 113
<212> PRT
<213> Rattus rattus

<400> 14

Phe Pro Pro Thr Phe Lys Glu Thr Ser Gln Leu Lys Thr Lys Leu Pro
1 5 10 15

Glu Asn Leu Ser Ser Lys Ile Lys Leu Leu Gln Leu Tyr Ser Glu Ala
20 25 30

Ser Val Ala Leu Leu Lys Leu Asn Asn Pro Lys Gly Phe Pro Glu Leu
35 40 45

Asn Lys Gln Thr Lys Lys Asn Met Ser Ile Ser Gly Lys Glu Leu Ala
50 55 60

Ile Ser Pro Ala Tyr Leu Leu Trp Asp Leu Ser Ala Ile Ser Gln Ser
65 70 75 80

Lys Gln Asp Glu Asp Val Ser Ala Ser Arg Phe Glu Asp Asn Glu Glu
85 90 95

Leu Arg Tyr Ser Leu Arg Ser Ile Glu Arg His Asp Ser Met Ser Pro
100 105 110

Leu

<210> 15
<211> 1105
<212> DNA
<213> Drosophila melanogaster

<220>
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<222> (903)..(903)
<223> n is a, g, t, or c

<220>
<221> misc_feature
<222> (935)..(935)
<223> n is a, g, t, or c

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<221> misc_feature
<222> (1023)..(1023)
<223> n is a, g, t, or c

<220>
<221> misc_feature
<222> (1035)..(1035)
<223> n is a, g, t, or c

<220>
<221> misc_feature
<222> (1071)..(1071)
<223> n is a, g, t, or c

<220>
<221> misc_feature
<222> (1100)..(1100)
<223> n is a, g, t, or c

<400> 15

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tccctggaaa aacacgccgc atggatcagg catgtgtaca tagtaaccaa tggccagatt     120

ccaagttggc tggatctcag ctacgaaagg gtcacggtgg tgccccacga agtcctggct     180

cccgatcccg accagctgcc caccttctcc agctcggcca tcgagacatt tctgcaccgc     240

ataccaaagc tgtccaagag gttcctctac ctcaacgacg acatattcct gggagctccg     300

ctgtatccgg aggacttgta cactgaagcg gagggagttc gcgtgtacca ggcatggatg     360

gtgcccggct gcgccttgga ttgcccctgg acgtacatag gtgatggagc ttgcgatcgg     420

cactgcaaca ttgatgcgtg ccaatttgat ggaggcgact gcagtgaaac tgggccagcg     480

agcgatgccc acgtcattcc accaagcaaa gaagtgctcg aggtgcagcc tgccgctgtt     540

ccacaatcaa gagtccaccg atttcctcag atgggtctcc aaaagctgtt caggcgcagc     600

tctgccaatt ttaaggatgt tatgcggcac cgcaatgtgt ccacactcaa ggaactacgt     660

cgcattgtgg agcgttttaa caaggccaaa ctcatgtcgc tgaaccccga actggagacc     720

tccagctccg agccacagac aactcagcgc cacgggctgc gcaaggagga ttttaagtct     780

tccaccgata tttactctca ctcgctgatt gccaccaata tgttgctgaa tagagcctat     840

ggctttaagg cacgccatgt cctggcgcac gtgggcttcc taattgacaa ggatattgtg     900

gangccatgc aacgacgttt taccagcgaa ttctngacac tggccattaa cgctttccga     960

gccccaacag atttgcagta cgcattcgct tactacttct ttctaatgag cgaaatccaa    1020

gtnatgagtg tagangaaat cttcgatgaa gtcgacaccg gacggtttgg ncacctggtc    1080

ggatccagaa gtgcgaaccn tttta                                          1105
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<210> 16
<211> 502
<212> PRT

<213> Drosophila melanogaster

<400> 16

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Gly Thr Arg Arg Phe Asp Asp Lys Asn Glu Leu Arg Tyr Ser Leu Arg
1               5                  10                  15

Ser Leu Glu Lys His Ala Ala Trp Ile Arg His Val Tyr Ile Val Thr
            20                  25                  30

Asn Gly Gln Ile Pro Ser Trp Leu Asp Leu Ser Tyr Glu Arg Val Thr
        35                  40                  45

Val Val Pro His Glu Val Leu Ala Pro Asp Pro Asp Gln Leu Pro Thr
    50                  55                  60

Phe Ser Ser Ser Ala Ile Glu Thr Phe Leu His Arg Ile Pro Lys Leu
65                  70                  75                  80

Ser Lys Arg Phe Leu Tyr Leu Asn Asp Asp Ile Phe Leu Gly Ala Pro
                85                  90                  95

Leu Tyr Pro Glu Asp Leu Tyr Thr Glu Ala Glu Gly Val Arg Val Tyr
            100                 105                 110

Gln Ala Trp Met Val Pro Gly Cys Ala Leu Asp Cys Pro Trp Thr Tyr
        115                 120                 125

Ile Gly Asp Gly Ala Cys Asp Arg His Cys Asn Ile Asp Ala Cys Gln
    130                 135                 140

Phe Asp Gly Gly Asp Cys Ser Glu Thr Gly Pro Ala Ser Asp Ala His
145                 150                 155                 160

Val Ile Pro Pro Ser Lys Glu Val Leu Glu Val Gln Pro Ala Ala Val
                165                 170                 175

Pro Gln Ser Arg Val His Arg Phe Pro Gln Met Gly Leu Gln Lys Leu
            180                 185                 190

Phe Arg Arg Ser Ser Ala Asn Phe Lys Asp Val Met Arg His Arg Asn
        195                 200                 205

Val Ser Thr Leu Lys Glu Leu Arg Arg Ile Val Glu Arg Phe Asn Lys
```

```
    210                 215                 220

Ala Lys Leu Met Ser Leu Asn Pro Glu Leu Glu Thr Ser Ser Ser Glu
225                 230                 235                 240

Pro Gln Thr Thr Gln Arg His Gly Leu Arg Lys Glu Asp Phe Lys Ser
                245                 250                 255

Ser Thr Asp Ile Tyr Ser His Ser Leu Ile Ala Thr Asn Met Leu Leu
            260                 265                 270

Asn Arg Ala Tyr Gly Phe Lys Ala Arg His Val Leu Ala His Val Gly
        275                 280                 285

Phe Leu Ile Asp Lys Asp Ile Val Glu Ala Met Gln Arg Arg Phe His
    290                 295                 300

Gln Gln Ile Leu Asp Thr Ala His Gln Arg Phe Arg Ala Pro Thr Asp
305                 310                 315                 320

Leu Gln Tyr Ala Phe Ala Tyr Tyr Ser Phe Leu Met Ser Glu Thr Lys
                325                 330                 335

Val Met Ser Val Glu Glu Ile Phe Asp Glu Phe Asp Thr Asp Gly Ser
            340                 345                 350

Ala Thr Trp Ser Asp Arg Glu Val Arg Thr Phe Leu Thr Arg Ile Tyr
        355                 360                 365

Gln Pro Pro Leu Asp Trp Ser Ala Met Arg Tyr Phe Glu Glu Val Val
    370                 375                 380

Gln Asn Cys Thr Arg Asn Leu Gly Met His Leu Lys Val Asp Thr Val
385                 390                 395                 400

Glu His Ser Thr Leu Val Tyr Glu Arg Tyr Glu Asp Ser Asn Leu Pro
                405                 410                 415

Thr Ile Thr Arg Asp Leu Val Val Arg Cys Pro Leu Leu Ala Glu Ala
            420                 425                 430

Leu Ala Ala Asn Phe Ala Val Arg Pro Lys Tyr Asn Phe His Val Ser
        435                 440                 445
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Pro Lys Arg Thr Ser His Ser Asn Phe Met Met Leu Thr Ser Asn Leu
450 455 460

Thr Glu Val Val Glu Ser Leu Asp Arg Leu Arg Arg Asn Pro Arg Lys
465 470 475 480

Phe Asn Cys Ile Asn Asp Asn Leu Asp Ala Asn Arg Gly Glu Asp Asn
485 490 495

Glu Asp Gly Ala Pro Ser
500

<210> 17
<211> 2183
<212> DNA
<213> Homo sapiens

<400> 17
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gaagcgtccg gcggcctcga ctcgggggcc tcccgcgacg acgacttgct actgccctat 120

ccacgcgcgc gcgcgcgcct cccccgggac tgcacacggg tgcgcgccgg caaccgcgag 180

cacgagagtt ggcctccgcc tcccgcgact cccggcgccg gcggtctggc cgtgcgcacc 240

ttcgtgtcgc acttcaggga ccgcgcggtg gccggccacc tgacgcgggc cgttgagccc 300

ctgcgcacct tctcggtgct ggagcccggt ggacccggcg gctgcgcggc gagacgacgc 360

gccaccgtgg aggagacggc gcgggcggcc gactgccgtg tcgcccagaa cggcggcttc 420

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agctccgggg ggctgcagaa cgcgcagttc gggatccgcc gcgacgggac cctggtcacc 540

gggtacctgt ctgaggagga ggtgctggac actgagaacc catttgtgca gctgctgagt 600

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gactgtggcc cctctaactg cagccagcac ggactgtgca cggagaccgg ctgccgctgt 1140

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tgcagcgtct ccagagtaaa gcagtgtctc agccacctg aagccaccct gagggcggga 1320

gaactctcct ttttcaccag gaccgcctgg ctagccctca ccctggcgct ggccttcctc 1380

ctgctgatca gcattgcagc aaacctgtcc ttgctcctgt ccagagcaga gaggaaccgg 1440

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gcagagaagg agcagccagg gggcgcccac aacccccttca aggactgaag cctcaagctg 1560

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tcctgatagc acttgtgcct cagcccctca cctggccacc tgccagggca cctgcaaccc 1740

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tggccagcac ccctggctgg agtgggttaa agggacgagt ctgccttcct ggctgtgaca 1980

cgggacccct tttctacaga cctcatcact ggatttgcca actagaattc gatttcctgt 2040

cataggaagc tccttggaag aagggatggg gggatgaaat catgtttaca gacctgtttt 2100

gtcatcctgc tgccaagaag ttttttaatc acttgaataa attgatataa taaaaggagc 2160

caccaggtgg tgtgtggatt ctg 2183

<210> 18
<211> 515
<212> PRT
<213> Homo sapiens

<400> 18

Met Ala Thr Ser Thr Gly Arg Trp Leu Leu Leu Arg Leu Ala Leu Phe
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Gly Phe Leu Trp Glu Ala Ser Gly Gly Leu Asp Ser Gly Ala Ser Arg
20 25 30

Asp Asp Asp Leu Leu Leu Pro Tyr Pro Arg Ala Arg Ala Arg Leu Pro
35 40 45

Arg Asp Cys Thr Arg Val Arg Ala Gly Asn Arg Glu His Glu Ser Trp
50 55 60

Pro Pro Pro Pro Ala Thr Pro Gly Ala Gly Gly Leu Ala Val Arg Thr
65 70 75 80

Phe Val Ser His Phe Arg Asp Arg Ala Val Ala Gly His Leu Thr Arg
85 90 95

Ala Val Glu Pro Leu Arg Thr Phe Ser Val Leu Glu Pro Gly Gly Pro
100 105 110

Gly Gly Cys Ala Ala Arg Arg Arg Ala Thr Val Glu Glu Thr Ala Arg
115 120 125

Ala Ala Asp Cys Arg Val Ala Gln Asn Gly Gly Phe Phe Arg Met Asn
130 135 140

Ser Gly Glu Cys Leu Gly Asn Val Val Ser Asp Glu Arg Arg Val Ser
145 150 155 160

Ser Ser Gly Gly Leu Gln Asn Ala Gln Phe Gly Ile Arg Arg Asp Gly
165 170 175

Thr Leu Val Thr Gly Tyr Leu Ser Glu Glu Glu Val Leu Asp Thr Glu
180 185 190

Asn Pro Phe Val Gln Leu Leu Ser Gly Val Val Trp Leu Ile Arg Asn
195 200 205

Gly Ser Ile Tyr Ile Asn Glu Ser Gln Ala Thr Glu Cys Asp Glu Thr
210 215 220

Gln Glu Thr Gly Ser Phe Ser Lys Phe Val Asn Val Ile Ser Ala Arg
225 230 235 240

Thr Ala Ile Gly His Asp Arg Lys Gly Gln Leu Val Leu Phe His Ala
245 250 255

Asp Gly His Thr Glu Gln Arg Gly Ile Asn Leu Trp Glu Met Ala Glu

260 265 270

Phe Leu Leu Lys Gln Asp Val Val Asn Ala Ile Asn Leu Asp Gly Gly
275 280 285

Gly Ser Ala Thr Phe Val Leu Asn Gly Thr Leu Ala Ser Tyr Pro Ser
290 295 300

Asp His Cys Gln Asp Asn Met Trp Arg Cys Pro Arg Gln Val Ser Thr
305 310 315 320

Val Val Cys Val His Glu Pro Arg Cys Gln Pro Pro Asp Cys His Gly
325 330 335

His Gly Thr Cys Val Asp Gly His Cys Gln Cys Thr Gly His Phe Trp
340 345 350

Arg Gly Pro Gly Cys Asp Glu Leu Asp Cys Gly Pro Ser Asn Cys Ser
355 360 365

Gln His Gly Leu Cys Thr Glu Thr Gly Cys Arg Cys Asp Ala Gly Trp
370 375 380

Thr Gly Ser Asn Cys Ser Glu Glu Cys Pro Leu Gly Trp His Gly Pro
385 390 395 400

Gly Cys Gln Arg Arg Cys Lys Cys Glu His His Cys Pro Cys Asp Pro
405 410 415

Lys Thr Gly Asn Cys Ser Val Ser Arg Val Lys Gln Cys Leu Gln Pro
420 425 430

Pro Glu Ala Thr Leu Arg Ala Gly Glu Leu Ser Phe Phe Thr Arg Thr
435 440 445

Ala Trp Leu Ala Leu Thr Leu Ala Leu Ala Phe Leu Leu Leu Ile Ser
450 455 460

Ile Ala Ala Asn Leu Ser Leu Leu Leu Ser Arg Ala Glu Arg Asn Arg
465 470 475 480

Arg Leu His Gly Asp Tyr Ala Tyr His Pro Leu Gln Glu Met Asn Gly
485 490 495

Glu Pro Leu Ala Ala Glu Lys Glu Gln Pro Gly Gly Ala His Asn Pro
500 505 510

Phe Lys Asp
515

<210> 19
<211> 2005
<212> DNA
<213> Mus musculus

<400> 19
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gactgcgccc gggtgcgctc aggtagccca gagcaggaga gctggcctcc gccacctctg 120

gccacccacg aaccccgggc gccaagccac cacgcggccg tgcgcacctt cgtgtcgcac 180

ttcgaggggc gcgcggtggc cggccacctg acgcgggtcg ccgatcccct acgcactttc 240

tcggtgctgg agcccggagg agccgggggc tgcggcggca gaagcgccgc ggctactgtg 300

gaggacacag ccgtccgggc cggttgccgc atcgctcaga acggtggctt cttccgcatg 360

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cttgaagaag aggttctgga tcccgtgaat ccgttcgtgc agctgctgag cggagtcgtg 540

tggctcatcc gcaatggaaa catctacatc aacgagagcc aagccatcga gtgtgacgag 600

acacaggaga caggttcttt tagcaaattt gtgaatgtga tgtcagccag gacagccgtg 660

ggtcatgacc gtgaggggca gcttatcctc ttccatgctg atggacagac ggaacagcgt 720

ggccttaacc tatgggagat ggcagagttc ctgcgtcaac aagatgtcgt caatgccatc 780

aacctggatg gaggcggttc tgctactttt gtgctcaatg ggaccctggc cagttaccct 840

tcagatcact gccaggacaa catgtggcgc tgtccccgcc aagtgtccac tgtggtgtgt 900

gtgcatgaac cgcgctgcca gccacccgac tgcagtggcc atgggacctg tgtggatggc 960

cactgtgaat gcaccagcca cttctggcgg ggcgaggcct gcagcgagct ggactgtggc 1020

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